

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:40:18 ; Search time 3651 Seconds
(without alignments)
14222.654 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272
1 gaattcggttcacccgcg.....acaccagaagtaagaattc 1272

Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Scoring table: 45554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA Main:*

- 1: /cgn2_6/prodata/1/pna/PCPUS1_COMB.seq:*
- 2: /cgn2_6/prodata/1/pna/PCPUS2_COMB.seq:*
- 3: /cgn2_6/prodata/1/pna/PCPUS3_COMB.seq:*
- 4: /cgn2_6/prodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/prodata/1/pna/US07_COMB.seq:*
- 6: /cgn2_6/prodata/1/pna/US08_COMB.seq:*
- 7: /cgn2_6/prodata/1/pna/US081_COMB.seq:*
- 8: /cgn2_6/prodata/1/pna/US082_COMB.seq:*
- 9: /cgn2_6/prodata/1/pna/US083_COMB.seq:*
- 10: /cgn2_6/prodata/1/pna/US084_COMB.seq:*
- 11: /cgn2_6/prodata/1/pna/US085_COMB.seq:*
- 12: /cgn2_6/prodata/1/pna/US086_COMB.seq:*
- 13: /cgn2_6/prodata/1/pna/US087_COMB.seq:*
- 14: /cgn2_6/prodata/1/pna/US088_COMB.seq:*
- 15: /cgn2_6/prodata/1/pna/US089_COMB.seq:*
- 16: /cgn2_6/prodata/1/pna/US090_COMB.seq:*
- 17: /cgn2_6/prodata/1/pna/US091_COMB.seq:*
- 18: /cgn2_6/prodata/1/pna/US092A_COMB.seq:*
- 19: /cgn2_6/prodata/1/pna/US092B_COMB.seq:*
- 20: /cgn2_6/prodata/1/pna/US093A_COMB.seq:*
- 21: /cgn2_6/prodata/1/pna/US093B_COMB.seq:*
- 22: /cgn2_6/prodata/1/pna/US094_COMB.seq:*
- 23: /cgn2_6/prodata/1/pna/US095A_COMB.seq:*
- 24: /cgn2_6/prodata/1/pna/US095B_COMB.seq:*
- 25: /cgn2_6/prodata/1/pna/US095C_COMB.seq:*
- 26: /cgn2_6/prodata/1/pna/US095D_COMB.seq:*
- 27: /cgn2_6/prodata/1/pna/US096A_COMB.seq:*
- 28: /cgn2_6/prodata/1/pna/US096B_COMB.seq:*
- 29: /cgn2_6/prodata/1/pna/US096C_COMB.seq:*
- 30: /cgn2_6/prodata/1/pna/US096D_COMB.seq:*
- 31: /cgn2_6/prodata/1/pna/US096E_COMB.seq:*
- 32: /cgn2_6/prodata/1/pna/US097A_COMB.seq:*
- 33: /cgn2_6/prodata/1/pna/US097B_COMB.seq:*
- 34: /cgn2_6/prodata/1/pna/US097C_COMB.seq:*
- 35: /cgn2_6/prodata/1/pna/US098A_COMB.seq:*
- 36: /cgn2_6/prodata/1/pna/US098B_COMB.seq:*
- 37: /cgn2_6/prodata/1/pna/US098C_COMB.seq:*
- 38: /cgn2_6/prodata/1/pna/US098D_COMB.seq:*
- 39: /cgn2_6/prodata/1/pna/US099A_COMB.seq:*
- 40: /cgn2_6/prodata/1/pna/US099B_COMB.seq:*
- 41: /cgn2_6/prodata/1/pna/US099C_COMB.seq:*
- 42: /cgn2_6/prodata/1/pna/US099D_COMB.seq:*
- 43: /cgn2_6/prodata/1/pna/US099E_COMB.seq:*

- 44: /cgn2_6/prodata/1/pna/US099F_COMB.seq:*
- 45: /cgn2_6/prodata/1/pna/US099G_COMB.seq:*
- 46: /cgn2_6/prodata/1/pna/US100A_COMB.seq:*
- 47: /cgn2_6/prodata/1/pna/US100B_COMB.seq:*
- 48: /cgn2_6/prodata/1/pna/US101A_COMB.seq:*
- 49: /cgn2_6/prodata/1/pna/US101B_COMB.seq:*
- 50: /cgn2_6/prodata/1/pna/US102A_COMB.seq:*
- 51: /cgn2_6/prodata/1/pna/US102B_COMB.seq:*
- 52: /cgn2_6/prodata/1/pna/US103A_COMB.seq:*
- 53: /cgn2_6/prodata/1/pna/US103B_COMB.seq:*
- 54: /cgn2_6/prodata/1/pna/US104A_COMB.seq:*
- 55: /cgn2_6/prodata/1/pna/US104B_COMB.seq:*
- 56: /cgn2_6/prodata/1/pna/US105A_COMB.seq:*
- 57: /cgn2_6/prodata/1/pna/US105B_COMB.seq:*
- 58: /cgn2_6/prodata/1/pna/US106A_COMB.seq:*
- 59: /cgn2_6/prodata/1/pna/US107A_COMB.seq:*
- 60: /cgn2_6/prodata/1/pna/US107B_COMB.seq:*
- 61: /cgn2_6/prodata/1/pna/US107C_COMB.seq:*
- 62: /cgn2_6/prodata/1/pna/US107D_COMB.seq:*
- 63: /cgn2_6/prodata/1/pna/US108A_COMB.seq:*
- 64: /cgn2_6/prodata/1/pna/US108B_COMB.seq:*
- 65: /cgn2_6/prodata/1/pna/US109A_COMB.seq:*
- 66: /cgn2_6/prodata/1/pna/US109B_COMB.seq:*
- 67: /cgn2_6/prodata/1/pna/US109C_COMB.seq:*
- 68: /cgn2_6/prodata/1/pna/US110_COMB.seq:*
- 69: /cgn2_6/prodata/1/pna/US6000_COMB.seq:*
- 70: /cgn2_6/prodata/1/pna/US6001_COMB.seq:*
- 71: /cgn2_6/prodata/1/pna/US6002_COMB.seq:*
- 72: /cgn2_6/prodata/1/pna/US6003_COMB.seq:*
- 73: /cgn2_6/prodata/1/pna/US6004_COMB.seq:*
- 74: /cgn2_6/prodata/1/pna/US6005_COMB.seq:*
- 75: /cgn2_6/prodata/1/pna/US6006_COMB.seq:*
- 76: /cgn2_6/prodata/1/pna/US6007_COMB.seq:*
- 77: /cgn2_6/prodata/1/pna/US6008_COMB.seq:*
- 78: /cgn2_6/prodata/1/pna/US6009_COMB.seq:*
- 79: /cgn2_6/prodata/1/pna/US6010_COMB.seq:*
- 80: /cgn2_6/prodata/1/pna/US6011_COMB.seq:*
- 81: /cgn2_6/prodata/1/pna/US6012_COMB.seq:*
- 82: /cgn2_6/prodata/1/pna/US6013_COMB.seq:*
- 83: /cgn2_6/prodata/1/pna/US6014_COMB.seq:*
- 84: /cgn2_6/prodata/1/pna/US6015_COMB.seq:*
- 85: /cgn2_6/prodata/1/pna/US6016_COMB.seq:*
- 86: /cgn2_6/prodata/1/pna/US6017_COMB.seq:*
- 87: /cgn2_6/prodata/1/pna/US6018_COMB.seq:*
- 88: /cgn2_6/prodata/1/pna/US6019_COMB.seq:*
- 89: /cgn2_6/prodata/1/pna/US6020_COMB.seq:*
- 90: /cgn2_6/prodata/1/pna/US6021_COMB.seq:*
- 91: /cgn2_6/prodata/1/pna/US6022_COMB.seq:*
- 92: /cgn2_6/prodata/1/pna/US6023A_COMB.seq:*
- 93: /cgn2_6/prodata/1/pna/US6023B_COMB.seq:*
- 94: /cgn2_6/prodata/1/pna/US6024_COMB.seq:*
- 95: /cgn2_6/prodata/1/pna/US6025_COMB.seq:*
- 96: /cgn2_6/prodata/1/pna/US6026_COMB.seq:*
- 97: /cgn2_6/prodata/1/pna/US6027_COMB.seq:*
- 98: /cgn2_6/prodata/1/pna/US6028_COMB.seq:*
- 99: /cgn2_6/prodata/1/pna/US6029_COMB.seq:*
- 100: /cgn2_6/prodata/1/pna/US6030_COMB.seq:*
- 101: /cgn2_6/prodata/1/pna/US6031_COMB.seq:*
- 102: /cgn2_6/prodata/1/pna/US6032_COMB.seq:*
- 103: /cgn2_6/prodata/1/pna/US6033_COMB.seq:*
- 104: /cgn2_6/prodata/1/pna/US6034_COMB.seq:*
- 105: /cgn2_6/prodata/1/pna/US6035_COMB.seq:*
- 106: /cgn2_6/prodata/1/pna/US6036_COMB.seq:*
- 107: /cgn2_6/prodata/1/pna/US6037_COMB.seq:*
- 108: /cgn2_6/prodata/1/pna/US6038_COMB.seq:*
- 109: /cgn2_6/prodata/1/pna/US6039_COMB.seq:*
- 110: /cgn2_6/prodata/1/pna/US6040_COMB.seq:*
- 111: /cgn2_6/prodata/1/pna/US6041_COMB.seq:*
- 112: /cgn2_6/prodata/1/pna/US6042_COMB.seq:*
- 113: /cgn2_6/prodata/1/pna/US6043_COMB.seq:*
- 114: /cgn2_6/prodata/1/pna/US6044_COMB.seq:*
- 115: /cgn2_6/prodata/1/pna/US6045_COMB.seq:*
- 116: /cgn2_6/prodata/1/pna/US6046_COMB.seq:*

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 02:16:03 / Search time 1341 Seconds
(without alignments)
4061.146 Million cell updates/sec

Title: US-10-077-111-13
Perfect score: 2047
Sequence: 1 MVKLITLADHGDVNCFA.....LTPNRLKMAINRWLETHOK 384

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 26938570 seqs, 7091142127 residues

Total number of hits satisfying chosen parameters: 53877140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+;p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US10077111/runatc_24102005_072847_8258/app_query.fasta.1.583
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.ccl
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10077111.OCGN_1_141 @runatc_24102005_072847_8258 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2:*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1:*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq10:*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq11:*
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq12:*
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq13:*
13: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq14:*
14: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq15:*
15: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq16:*
16: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq17:*
17: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq18:*
18: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq19:*
19: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq20:*
20: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq21:*
21: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq22:*
22: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq23:*
23: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq24:*
24: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq25:*
25: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq26:*
26: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq27:*
27: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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Thu Oct 25 11:58:42 2005

us-10-077-111-12.rnpn

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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:49:01 ; Search time 5929 Seconds
(without alignments)
3067.275 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272

Sequence: 1 gaattcggtcttaccctgcg.....acaccacaagtaagaattc 1272

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27700967 seqs, 7148534824 residues

Total number of hits satisfying chosen parameters: 55401934

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
- 2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
- 3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*
- 8: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
- 9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq10:*
- 11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq11:*
- 12: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq1:*
- 13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
- 14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*
- 15: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq5:*
- 16: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq6:*
- 17: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq7:*
- 18: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq8:*
- 19: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq9:*
- 20: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
- 21: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
- 22: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*
- 23: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq4:*
- 24: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq5:*
- 25: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq6:*
- 26: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq7:*
- 27: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			
No.	Score	Query	Description
		Match Length DB ID	

117: /cgn2_6/prodata/1/pna/US6047_COMB.seq:*
 118: /cgn2_6/prodata/1/pna/US6048_COMB.seq:*
 119: /cgn2_6/prodata/1/pna/US6049_COMB.seq:*
 120: /cgn2_6/prodata/1/pna/US6050_COMB.seq:*
 121: /cgn2_6/prodata/1/pna/US6051_COMB.seq:*
 122: /cgn2_6/prodata/1/pna/US6052_COMB.seq:*
 123: /cgn2_6/prodata/1/pna/US6053_COMB.seq:*
 124: /cgn2_6/prodata/1/pna/US6054_COMB.seq:*
 125: /cgn2_6/prodata/1/pna/US6055_COMB.seq:*
 126: /cgn2_6/prodata/1/pna/US6056_COMB.seq:*
 127: /cgn2_6/prodata/1/pna/US6057_COMB.seq:*
 128: /cgn2_6/prodata/1/pna/US6058_COMB.seq:*
 129: /cgn2_6/prodata/1/pna/US6059_COMB.seq:*

RP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*
117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
118: /cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
119: /cgn2_6/ptodata/1/pna/US6049_COMB.seq:*
120: /cgn2_6/ptodata/1/pna/US6050_COMB.seq:*
121: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
122: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
123: /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
124: /cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
125: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
126: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
127: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
128: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 02:08:13 ; Search time 3255 Seconds
(without alignments)
4815,990 Million cell updates/sec

Title: us-10-077-111-13

Perfect score: 2047
Sequence: 1 MVVLHTLADHDVNCACF.....LTPNRLKMAINRWLETHQK 384

Scoring table:

BL0SUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 4554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODELS=frame+ p2n.model -DEV=xlh
-O/cg2_1/USFTO.spool/US10077111.rnrmc_24102005_072847_8228/app.query.fasta.1.583
-DB=Pending_Patents_NA_Main -QMT=fastap -SUFFIX=irmpm -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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SUMMARIES

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13	430	33.8	147021	9	AC006501 Homo sapi
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C 25	297	23.3	297	6	CO148540
C 26	297	23.3	297	6	CO231810
C 27	297	23.3	297	6	CO307124
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C 31	275.4	21.7	196403	2	AC102767
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ALIGNMENTS

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LOCUS	BC029520				
DEFINITION	Homo sapiens WD repeat and SAM domain containing 1, mRNA (cDNA clone MGC:33855 IMAGE:5301559), complete cds.				
ACCESSION	BC029520.1	GI:20810486			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1564)				
AUTHORS	Klausner, R.D., Collins, P.S., Wagner, L., Shemen, C.M., Schler, G.D., Altschul, S.F., Zeeberg, B., Buecaw, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, Y., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavani, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tashy, S., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.U., Mckernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Huijck, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, B., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakeley, R.W., Touchman, D.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Dickey, J., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PubMed	12477932				
REFERENCE	2 (bases 1 to 1564)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submissions				
JOURNAL	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA				

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ALIGNMENTS

LOCUS	1564 bp	mRNA	linear	PRI 20-JUL-2004
DEFINITION	Homo sapiens WD repeat and SAM domain containing 1, mRNA (CDNA clone MGC:33855 IMAGE:530155), complete cds.			
ACCESSION	BC029520			
VERSION	BC029520.1			
KEYWORDS	MGC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Bukacynska, Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia, Eutheria, Primates: Catarrhini: Homnidae; Homo. 1 (bases 1 to 1564)			
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, K.L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.C., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hultk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettrem, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A.C., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesteley, R.W., Touchman, J.W., Green, E.D.,			

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RESULT 2	LOCUS	SEQUENCE	DEFINITION
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	Sequence 23179	from Patent WO0100860.	PAT 30-JAN-2004
	CQ491312		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
use

JOURNAL Patent: WO 010860-A 23/1/9 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES Location/Qualifiers

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US-10-077-111-13 (1-384) x CQ491312 (1-1996)

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Db 256 TGGAACTACTGAAAAATGGACACATCTCTGGCAGTATATGGAAACAGCCCTAGTGTGGCAGCCCTCTG 315

Db 316 AGGGTTGGCAGTTTCCCAAGACTCCAGTGTGGCATCAGGGGACAGTGTGGAAT 375

QY 121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValIlysAspCly 140

Db 376 GTCGTTTGTGGAAATGCACACTCATACAAATTTATATAGTGTGGTAGTGTTTAAAGATGC 435

QY 14 SELDEKATATAACYNAAIDFUSEI FLOMSNGYSEL FNEUNEVALINIGYSEL SELCYLS 100

Ddb 436 TCTTTGGCGGCAATGECATTTCCTTCATGGAAGCTTCTTTGTACTGCTCTCATGT 435

OY	16	GlyAspLeuThrVal	1	TrpAspAspLeuMetArgCysLeuH1AspSerGluLysVal	180
Db	496	GGGATATTAACAGTGTGGATGATAAATAAGAGTGTCTCAATGTAAGAAACACACTGAT	555		
OY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu	200		
Db	556	CTTGGAAATTAACCTGGCTGGCATTTTCTTCCAGCCAGCTTCTTGATGAGAACAAAGGCTCT	615		
OY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer	220		
Db	616	CAGTTTTTTCGACTGGCATCATGTGTGCAGGATTGGCAAGTTCGCAAAATTGGATTGTTTCT	675		
OY	221	PheThrHisIleLeu	225		
Db	676	TTTAACCCAATCTTAGGCTTTGGAATTAATAATATAAAGTACACTGAGTGGGACCTGTCT	735		
OY	225		225		
Db	736	CGTGTTCGTGCTTGTGCTTTTCCATGATAGGAGACAGTCTAGTCTCAGGTCAGTGAT	795		
OY	225		225		
Db	796	AAGTGTGTCATGATATATGATACTAATACTAGAGAATATATTCTTACACATTGACTGACAC	855		
OY	225		225		
Db	856	ACCAGGTATGTCAAACTGTGTCTTTTGCACCTAATACCTTTTACTTGCTCACTGCTTCA	915		
OY	226		226		
Db	916	ATGGAACAACCACTGAAACATCTGGCAATTGACCTGGAAACACTTGGCCACAGCAGGCC	975		
OY	229	ThrGluH1GlnLeuLysGlnPheThrGluAspTrpSerGluGluValValSerThrTrp	248		
Db	976	ACAGAACATCAGCTGGAAGCAATTATCCGGAAGATTGGCTCAGAGGAGGATCTTCACATG	1035		
OY	249	LeuCysValLeuLysPheLysAspLeuValGlyIlePheLysMetAspAsnIleAspGly	268		
Db	1036	CTTGTGTCAACAAGATTTAAAGATCTTGTGGATTTTCAAGATGAAATACATTGATGGA	1095		
OY	269	LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu	288		
Db	1096	AAGAACTGTGTAATCTTACAAAGAAAGCTGTGGCATGATTTGAAAAATTGATCTCTA	1155		
OY	289	GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu	308		
Db	1156	GGACTGCGTGTAAGGTGAGAGAAATTGAAGACTCAGGACCCAAAGGTTAAATCCCTT	1215		
OY	309	SerSerGlyLysLeuProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro	328		
Db	1216	TCTTCAGAAATCTCTGATGATTTAATATGTCACATACATGAGAACCTTATGAAAGATCCG	1275		
OY	329	ValIleAlaSerAspGlyLysSerTrpGluLysGluAlaMetGluAsnTrpIleSerLys	348		
Db	1276	GTCATGCCATCAAGATGCTATTATATGAAAAAGAACATGAAATTTGATCAGCAAA	1335		
OY	369	ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys	384		
Db	1396	AGGACTCTGAAAATGGCCATCAATTAATGATGGCTGAGACACACCAAAAG	1443		
RESULT 3					
LOCUS	CQ497179	1996 bp	DNA	linear	PAT 30-JAN-2004
DEFINITION	Sequence 29046 from Patent WO0160860.				
ACCESSION	CQ497179				
VERSION	CQ497179.1	GI:41462815			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				